Jude M Przyborski

List of Publications by Year
in descending order

76	2,995	172457	182427
papers	citations	29 h-index	51 g-index

78	78	78	2468
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Characterization of Plasmodium falciparum macrophage migration inhibitory factor homologue and its cysteine deficient mutants. Parasitology International, 2022, 87, 102513.	1.3	0
2	Structure and Function of Redox-Sensitive Superfolder Green Fluorescent Protein Variant. Antioxidants and Redox Signaling, 2022, 37, 1-18.	5.4	5
3	TLR8 is activated by 5Ê¹-methylthioinosine, a Plasmodium falciparum-derived intermediate of the purine salvage pathway. Cell Reports, 2022, 39, 110691.	6.4	6
4	Introductory Chapter: The Importance of Heat Shock Proteins in Survival and Pathogenesis of the Malaria Parasite Plasmodium falciparum. Advances in Experimental Medicine and Biology, 2021, 1340, 1-9.	1.6	1
5	Identification of sulfenylation patterns in trophozoite stage Plasmodium falciparum using a non-dimedone based probe. Molecular and Biochemical Parasitology, 2021, 242, 111362.	1.1	6
6	A nuclear protein, PfMORC confers melatonin dependent synchrony of the human malaria parasite P. falciparum in the asexual stage. Scientific Reports, 2021, 11, 2057.	3.3	10
7	Co-chaperone involvement in knob biogenesis implicates host-derived chaperones in malaria virulence. PLoS Pathogens, 2021, 17, e1009969.	4.7	9
8	A patatinâ€like phospholipase functions during gametocyte induction in the malaria parasite Plasmodium falciparum. Cellular Microbiology, 2020, 22, e13146.	2.1	21
9	Detection of the in vitro modulation of Plasmodium falciparum Arf1 by Sec7 and ArfGAP domains using a colorimetric plate-based assay. Scientific Reports, 2020, 10, 4193.	3.3	0
10	Partners in Mischief: Functional Networks of Heat Shock Proteins of Plasmodium falciparum and Their Influence on Parasite Virulence. Biomolecules, 2019, 9, 295.	4.0	31
11	Proteomic analysis of Plasmodium falciparum histone deacetylase 1 complex proteins. Experimental Parasitology, 2019, 198, 7-16.	1.2	8
12	Babesia divergens-infected red blood cells take up glutamate via an EAAT3 independent mechanism. International Journal of Medical Microbiology, 2018, 308, 148-154.	3.6	0
13	The N-terminal extension of the P. falciparum GBP130 signal peptide is irrelevant for signal sequence function. International Journal of Medical Microbiology, 2018, 308, 3-12.	3.6	5
14	Functional relevance of in vivo half antibody exchange of an IgG4 therapeutic antibody-drug conjugate. PLoS ONE, 2018, 13, e0195823.	2.5	16
15	A seven-helix protein constitutes stress granules crucial for regulating translation during human-to-mosquito transmission of Plasmodium falciparum. PLoS Pathogens, 2018, 14, e1007249.	4.7	22
16	Determination of glutathione redox potential and pH value in subcellular compartments of malaria parasites. Free Radical Biology and Medicine, 2017, 104, 104-117.	2.9	32
17	Trafficking of PfExp1 to the parasitophorous vacuolar membrane ofPlasmodium falciparumis independent of protein folding and the PTEX translocon. Cellular Microbiology, 2017, 19, e12710.	2.1	11
18	Plasmodium glyceraldehyde-3-phosphate dehydrogenase: A potential malaria diagnostic target. Experimental Parasitology, 2017, 179, 7-19.	1.2	25

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19	Proteomic analysis of exported chaperone/co-chaperone complexes of P. falciparum reveals an array of complex protein-protein interactions. Scientific Reports, 2017, 7, 42188.	3.3	38
20	Hydrogen peroxide dynamics in subcellular compartments of malaria parasites using genetically encoded redox probes. Scientific Reports, 2017, 7, 10449.	3.3	24
21	Genomic and Proteomic Evidence for the Presence of a Peroxisome in the Apicomplexan Parasite Toxoplasma gondii and Other Coccidia. Genome Biology and Evolution, 2017, 9, 3108-3121.	2.5	21
22	The exported chaperone Hsp70-x supports virulence functions for Plasmodium falciparum blood stage parasites. PLoS ONE, 2017, 12, e0181656.	2.5	45
23	Ticket to ride: export of proteins to the Plasmodium falciparumâ€infected erythrocyte. Molecular Microbiology, 2016, 101, 1-11.	2.5	21
24	Trafficking of the exported P. falciparum chaperone PfHsp70x. Scientific Reports, 2016, 6, 36174.	3.3	23
25	J-dot targeting of an exported HSP40 in Plasmodium falciparum-infected erythrocytes. International Journal for Parasitology, 2016, 46, 519-525.	3.1	29
26	Export of malaria proteins requires co-translational processing of the PEXEL motif independent of phosphatidylinositol-3-phosphate binding. Nature Communications, 2016, 7, 10470.	12.8	65
27	Toxoplasma gondii Toc75 Functions in Import of Stromal but not Peripheral Apicoplast Proteins. Traffic, 2015, 16, 1254-1269.	2.7	36
28	A WD40-repeat protein unique to malaria parasites associates with adhesion protein complexes and is crucial for blood stage progeny. Malaria Journal, 2015, 14, 435.	2.3	14
29	The apicomplexan parasiteBabesia divergensinternalizes band 3, glycophorin A and spectrin during invasion of human red blood cells. Cellular Microbiology, 2015, 17, 1052-1068.	2.1	21
30	Plasmodial HSP70s are functionally adapted to the malaria parasite life cycle. Frontiers in Molecular Biosciences, 2015, 2, 34.	3.5	45
31	Alternative Protein Secretion in the Malaria Parasite Plasmodium falciparum. PLoS ONE, 2015, 10, e0125191.	2.5	19
32	Plasmodium falciparum Hop (PfHop) Interacts with the Hsp70 Chaperone in a Nucleotide-Dependent Fashion and Exhibits Ligand Selectivity. PLoS ONE, 2015, 10, e0135326.	2.5	40
33	A Putative Non-Canonical Ras-Like GTPase from P. falciparum: Chemical Properties and Characterization of the Protein. PLoS ONE, 2015, 10, e0140994.	2.5	6
34	PFB0595w is a Plasmodium falciparum J protein that co-localizes with PfHsp70-1 and can stimulate its in vitro ATP hydrolysis activity. International Journal of Biochemistry and Cell Biology, 2015, 62, 47-53.	2.8	17
35	Identification and initial characterisation of a Plasmodium falciparum Cox17 copper metallochaperone. Experimental Parasitology, 2015, 148, 30-39.	1.2	10
36	Fractionation of Plasmodium-Infected Human Red Blood Cells to Study Protein Trafficking. Methods in Molecular Biology, 2015, 1270, 71-80.	0.9	10

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37	Prokaryotic ancestry and gene fusion of a dual localized peroxiredoxin in malaria parasites. Microbial Cell, 2015, 2, 5-13.	3.2	9
38	Protein Traffic to the Plasmodium falciparum Apicoplast: Evidence for a Sorting Branch Point at the Golgi. Traffic, 2014, 15, 1290-1304.	2.7	36
39	Use of self-assembling GFP to determine protein topology and compartmentalisation in the Plasmodium falciparum-infected erythrocyte. Molecular and Biochemical Parasitology, 2013, 187, 87-90.	1.1	13
40	Spatial association with PTEX complexes defines regions for effector export into Plasmodium falciparum-infected erythrocytes. Nature Communications, 2013, 4, 1415.	12.8	79
41	Characterization of Tt ALV2, an Essential Charged Repeat Motif Protein of the Tetrahymena thermophila Membrane Skeleton. Eukaryotic Cell, 2013, 12, 932-940.	3.4	17
42	Protein Traffic. , 2013, , 1-12.		0
43	Plasmodium falciparum-encoded exported hsp70/hsp40 chaperone/co-chaperone complexes within the host erythrocyte. Cellular Microbiology, 2012, 14, 1784-1795.	2.1	137
44	Wherever I may roam: Protein and membrane trafficking in P. falciparum-infected red blood cells. Molecular and Biochemical Parasitology, 2012, 186, 95-116.	1.1	56
45	Uncovering Common Principles in Protein Export of Malaria Parasites. Cell Host and Microbe, 2012, 12, 717-729.	11.0	115
46	Subcellular localization of adenylate kinases in Plasmodium falciparum. FEBS Letters, 2012, 586, 3037-3043.	2.8	16
47	Distribution of the SELMA Translocon in Secondary Plastids of Red Algal Origin and Predicted Uncoupling of Ubiquitin-Dependent Translocation from Degradation. Eukaryotic Cell, 2012, 11, 1472-1481.	3.4	58
48	Insight into the Selenoproteome of the Malaria ParasitePlasmodium falciparum. Antioxidants and Redox Signaling, 2012, 17, 534-543.	5.4	15
49	A Plasmodium falciparum copper-binding membrane protein with copper transport motifs. Malaria Journal, 2012, 11, 397.	2.3	25
50	Characterisation of the Plasmodium falciparum Hsp70â€“Hsp90 organising protein (PfHop). Cell Stress and Chaperones, 2012, 17, 191-202.	2.9	63
51	Intracellular Protozoan Parasites of Humans: The Role of Molecular Chaperones in Development and Pathogenesis. Protein and Peptide Letters, 2011, 18, 143-157.	0.9	115
52	Malaria proteases mediate inside-out egress of gametocytes from red blood cells following parasite transmission to the mosquito. Cellular Microbiology, 2011, 13, 897-912.	2.1	63
53	Plasmodium falciparum encodes a single cytosolic type I Hsp40 that functionally interacts with Hsp70 and is upregulated by heat shock. Cell Stress and Chaperones, 2011, 16, 389-401.	2.9	54
54	Two nucleusâ€localized CDKâ€like kinases with crucial roles for malaria parasite erythrocytic replication are involved in phosphorylation of splicing factor. Journal of Cellular Biochemistry, 2011, 112, 1295-1310.	2.6	44

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55	Protein biochemistry: Don't forget the cell biology. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 456.	2.3	3
56	Genetic Evidence Strongly Support an Essential Role for PfPV1 in Intra-Erythrocytic Growth of P. falciparum. PLoS ONE, 2011, 6, e18396.	2.5	23
57	The malaria parasite Plasmodium falciparum: cell biological peculiarities and nutritional consequences. Protoplasma, 2010, 240, 3-12.	2.1	16
58	Distinct subcellular localization in the cytosol and apicoplast, unexpected dimerization and inhibition of Plasmodium falciparum glyoxalases. Molecular Microbiology, 2010, 76, 92-103.	2.5	32
59	Parasite-encoded Hsp40 proteins define novel mobile structures in the cytosol of the P. falciparum-infected erythrocyte. Cellular Microbiology, 2010, 12, 1398-1420.	2.1	117
60	Compartmentation of Redox Metabolism in Malaria Parasites. PLoS Pathogens, 2010, 6, e1001242.	4.7	139
61	Recruitment of human aquaporin 3 to internal membranes in the Plasmodium falciparum infected erythrocyte. Molecular and Biochemical Parasitology, 2009, 167, 48-53.	1.1	27
62	Return to sender: use of Plasmodium ER retrieval sequences to study protein transport in the infected erythrocyte and predict putative ER protein families. Parasitology Research, 2009, 104, 1535-1541.	1.6	15
63	Protein unfolding is an essential requirement for transport across the parasitophorous vacuolar membrane of Plasmodium falciparum. Molecular Microbiology, 2009, 71, 613-628.	2.5	126
64	An Unusual ERAD-Like Complex Is Targeted to the Apicoplast ofPlasmodium falciparum. Eukaryotic Cell, 2009, 8, 1134-1145.	3.4	136
65	Protein Transport Across the Parasitophorous Vacuole of Plasmodium falciparum: Into the Great Wide Open. Traffic, 2008, 9, 157-165.	2.7	47
66	The Maurer's clefts of Plasmodium falciparum: parasite-induced islands within an intracellular ocean. Trends in Parasitology, 2008, 24, 285-288.	3.3	8
67	Der1-mediated Preprotein Import into the Periplastid Compartment of Chromalveolates?. Molecular Biology and Evolution, 2007, 24, 918-928.	8.9	142
68	Transport of nuclear-encoded proteins into secondarily evolved plastids. Biological Chemistry, 2007, 388, 899-906.	2.5	40
69	The long and winding road: Protein trafficking mechanisms in the Plasmodium falciparum infected erythrocyte. Molecular and Biochemical Parasitology, 2006, 147, 1-8.	1.1	47
70	Trafficking of STEVOR to the Maurer's clefts in Plasmodium falciparum-infected erythrocytes. EMBO Journal, 2005, 24, 2306-2317.	7.8	125
71	A single member of the Plasmodium falciparum var multigene family determines cytoadhesion to the placental receptor chondroitin sulphate A. EMBO Reports, 2005, 6, 775-781.	4.5	187
72	Willingness to pay for hypothetical malaria vaccines in rural Burkina Faso. Scandinavian Journal of Public Health, 2005, 33, 146-150.	2.3	33

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73	PARASITOLOGY: The Malarial Secretome. Science, 2004, 306, 1897-1898.	12.6	23
74	Recovery of adhesion to chondroitin-4-sulphate in Plasmodium falciparum var CSA disruption mutants by antigenically similar PfEMP1 variants. Molecular Microbiology, 2004, 49, 655-669.	2.5	28
75	The histone H4 gene of Plasmodium falciparum is developmentally transcribed in asexual parasites. Parasitology Research, 2003, 90, 387-389.	1.6	8
76	Maurerâ€™s cleftsâ€”a novel secretory organelle?. Molecular and Biochemical Parasitology, 2003, 132, 17-26.	1.1	64